Resource Summary Report

Generated by dkNET on Sep 14, 2026

RNA Modification Database

RRID:SCR_003535
Type: Tool

Proper Citation

RNA Modification Database (RRID:SCR_003535)

Resource Information

URL: http://mods.rna.albany.edu

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Description: The RNA modification database provides a comprehensive listing of posttranscriptionally modified nucleosides from RNA. Information provided for each nucleoside includes: the type of RNA in which it occurs and phylogenetic distribution; common chemical name and symbol; Chemical Abstracts registry number and index name; chemical structure; initial literature citations for structural characterization or occurrence, and for chemical synthesis. Both the structural diversity and extent of posttranscriptional modification in RNA is remarkable, with 107 different nucleosides presently known in all types of RNA. The discovery of new modified nucleosides as well as increasing knowledge of the array of functional roles of modification, based largely on extensive studies of tRNA, mandates a need for a comprehensive database of RNA nucleosides. The RNA Modification Database is maintained as an extension of the initial version published in mid-1994. The database consists of all RNA-derived ribonucleosides of known structure, including those from established sequence positions, as well as those detected or characterized from hydrolysates of RNA. The information provided permits access to the modified nucleoside literature through provision of both computer-searchable Chemical Abstracts registry numbers and key literature citations. This database also provides an historical record of the initial reports of occurrence, characterization and chemical synthesis of modified nucleosides from RNA. It is our judgement that the total number of RNA nucleosides listed, and the chemical structures reported, are very accurate. However, the distributions listed are in some cases a matter of concern, due primarily to the possibility of inhomogeneity of the RNA isolate and the use of methods of nucleoside identification that are not sufficiently rigorous. Reinvestigation of some of the unusual or single-report source distributions is warranted, and will likely lead to future refinements in the listings. The authors invite comments concerning new entries, errors or omissions and on the format presently used for electronic access to the database.

Abbreviations: RNAmods

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: PMID:9399834, PMID:9016519

Funding: NIGMS GM29812

Resource Name: RNA Modification Database

Resource ID: SCR_003535

Alternate IDs: nif-0000-03414

Old URLs: http://medlib.med.utah.edu/RNAmods/

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260912T195559+0000

Ratings and Alerts

No rating or validation information has been found for RNA Modification Database.

No alerts have been found for RNA Modification Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Liu WW, et al. (2024) RNA modifications in cellular metabolism: implications for metabolism-targeted therapy and immunotherapy. Signal transduction and targeted therapy, 9(1), 70.

Leptidis S, et al. (2022) Epitranscriptomics of cardiovascular diseases (Review). International journal of molecular medicine, 49(1).

Fu J, et al. (2021) The Role of m6A Ribonucleic Acid Modification in the Occurrence of Atherosclerosis. Frontiers in genetics, 12, 733871.

Anreiter I, et al. (2021) New Twists in Detecting mRNA Modification Dynamics. Trends in biotechnology, 39(1), 72.

Chujo T, et al. (2021) Human transfer RNA modopathies: diseases caused by aberrations in transfer RNA modifications. The FEBS journal, 288(24), 7096.

Berg MD, et al. (2021) Transfer RNAs: diversity in form and function. RNA biology, 18(3), 316.

Coureux PD, et al. (2020) Cryo-EM study of an archaeal 30S initiation complex gives insights into evolution of translation initiation. Communications biology, 3(1), 58.

Kulik K, et al. (2020) Different Oxidation Pathways of 2-Selenouracil and 2-Thiouracil, Natural Components of Transfer RNA. International journal of molecular sciences, 21(17).

Liu L, et al. (2020) Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. Computational and structural biotechnology journal, 18, 1587.

Leung J, et al. (2020) Who Rules the Cell? An Epi-Tale of Histone, DNA, RNA, and the Metabolic Deep State. Frontiers in plant science, 11, 181.

Lyu X, et al. (2020) Adaptation of codon usage to tRNA I34 modification controls translation kinetics and proteome landscape. PLoS genetics, 16(6), e1008836.

G?adysz M, et al. (2019) Thermodynamic and structural contributions of the 6-thioguanosine residue to helical properties of RNA. Scientific reports, 9(1), 4385.

McIntyre W, et al. (2018) Positive-sense RNA viruses reveal the complexity and dynamics of the cellular and viral epitranscriptomes during infection. Nucleic acids research, 46(11), 5776.

Tusup M, et al. (2018) Epitranscriptomics of cancer. World journal of clinical oncology, 9(3), 42.

Ng CS, et al. (2018) tRNA epitranscriptomics and biased codon are linked to proteome expression in Plasmodium falciparum. Molecular systems biology, 14(10), e8009.

Nilsson K, et al. (2017) An unmodified wobble uridine in tRNAs specific for Glutamine, Lysine, and Glutamic acid from Salmonella enterica Serovar Typhimurium results in nonviability-Due to increased missense errors? PloS one, 12(4), e0175092.

Jonkhout N, et al. (2017) The RNA modification landscape in human disease. RNA (New York, N.Y.), 23(12), 1754.

Sochacka E, et al. (2017) C5-substituents of uridines and 2-thiouridines present at the wobble position of tRNA determine the formation of their keto-enol or zwitterionic forms - a factor important for accuracy of reading of guanosine at the 3?-end of the mRNA codons. Nucleic acids research, 45(8), 4825.

Cai WM, et al. (2015) A Platform for Discovery and Quantification of Modified Ribonucleosides in RNA: Application to Stress-Induced Reprogramming of tRNA Modifications. Methods in enzymology, 560, 29.

Rose RE, et al. (2015) Profiling ribonucleotide modifications at full-transcriptome level: a step toward MS-based epitranscriptomics. RNA (New York, N.Y.), 21(7), 1361.